

SEQUENCE LISTING

<110> Ptacek, Louis J.
Fu, Ying-Hui
Jones, Christopher R.

<120> Casein Kinase I Delta and Casein Kinase I Epsilon and Sleep in
Humans

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Leu His Ile Glu Ser Lys Ile Tyr Lys Met Met Gln Gly Gly Val Gly
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Ser Arg Lys Phe Ser Leu Lys Thr Val Leu Leu Leu Ala Asp Gln Met
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Ile Ser Arg Ile Glu Tyr Ile His Ser Lys Asn Phe Ile His Arg Asp
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Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Ala Arg
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Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
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Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
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Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met Tyr Phe Asn Leu
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Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Ala Thr Lys Arg Gln Lys
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Asp Trp Asn Met Leu Lys Phe Gly Ala Ser Arg Ala Ala Asp Asp Ala
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Glu Arg Glu Arg Arg Asp Arg Glu Glu Arg Leu Arg His Ser Arg Asn
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Pro Ala Thr Arg Gly Leu Pro Ser Thr Ala Ser Gly Arg Leu Arg Gly
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Ala Asn Thr Ser Pro Arg Pro Val Ser Gly Met Glu Arg Glu Arg Lys
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Val Ser Met Arg Leu His Arg Gly Ala Pro Val Asn Ile Ser Ser Ser
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Leu His Ile Glu Ser Lys Ile Tyr Lys Met Met Gln Gly Gly Val Gly
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Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
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Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
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Tyr Glu Arg Ile Ser Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu
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Cys Lys Gly Tyr Pro Ser Glu Phe Ala Thr Tyr Leu Asn Phe Cys Arg
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Asp Trp Asn Met Leu Lys Phe Gly Ala Ser Arg Ala Ala Asp Asp Ala
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Pro Ala Thr Arg Gly Leu Pro Ser Thr Ala Ser Gly Arg Leu Arg Gly
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Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Ala Arg
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Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
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Val Ser Met Arg Leu His Arg Gly Ala Pro Val Asn Ile Ser Ser Ser
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Ile Pro Thr Ile Arg Trp Cys Gly Ala Glu Gly Asp Tyr Asn Val Met
65 70 75 80

Val Met Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys

85

90

95

Ser Arg Lys Phe Ser Leu Lys Thr Val Leu Leu Leu Ala Asp Gln Met
100 105 110

Ile Ser Arg Ile Glu Tyr Ile His Ser Lys Asn Phe Ile His Arg Asp
115 120 125

Val Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Lys Lys Gly Asn Leu
130 135 140

Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Ala Arg
145 150 155 160

Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
165 170 175

Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
180 185 190

Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met Tyr Phe Asn Leu
195 200 205

Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Ala Thr Lys Arg Gln Lys
210 215 220

Tyr Glu Arg Ile Ser Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu
225 230 235 240

Cys Lys Gly Tyr Pro Ser Glu Phe Ala Thr Tyr Leu Asn Phe Cys Arg
245 250 255

Ser Leu Arg Phe Asp Asp Lys Pro Asp Tyr Ser Tyr Leu Arg Gln Leu
260 265 270

Phe Arg Asn Leu Phe His Arg Gln Gly Phe Ser Tyr Asp Tyr Val Phe
275 280 285

Asp Trp Asn Met Leu Lys Phe Gly Ala Ser Arg Ala Ala Asp Asp Ala
290 295 300

Glu Arg Glu Arg Arg Asp Arg Glu Glu Arg Leu Arg His Ser Arg Asn
305 310 315 320

Pro Ala Thr Arg Gly Leu Pro Ser Thr Ala Ser Gly Arg Leu Arg Gly
 325 330 335

Thr Gln Glu Val Ala Pro Pro Thr Pro Leu Thr Pro Thr Ser His Thr
 340 345 350

Ala Asn Thr Ser Pro Arg Pro Val Ser Gly Met Glu Arg Glu Arg Lys
 355 360 365

Val Ser Met Arg Leu His Arg Gly Ala Pro Val Asn Ile Ser Ser Ser
 370 375 380

Asp Leu Thr Gly Arg Gln Asp Thr Ser Arg Met Ser Thr Ser Gln Asn
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Ser Ile Pro Phe Glu His His Gly Lys
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 <212> DNA
 <213> Homo sapiens

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ctacctgggt gccaacatcg cctctgggtga ggaagtgcgc atcaagctgg agtgtgtgaa	360
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gctgctgggg cctagcctcg aggacctgtt caacttctgt tcccccaat tcagcctcaa	540
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cttcatccac cgggacgtca agcccgacaa cttccatcg gggctggggaa agaaggccaa	660
cctggtctac atcatcgact tcggcctggc caagaagtac cgggacgccc gcacccacca	720
gcacattccc taccggaaaa acaagaacct gaccggcacg gccccgtacg cttccatcaa	780

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 <211> 416
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Ser Gly Ser Phe Gly Asp Ile Tyr Leu Gly Ala Asn Ile Ala Ser Gly
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Glu Glu Val Ala Ile Lys Leu Glu Cys Val Lys Thr Lys His Pro Gln
 35 40 45

Leu His Ile Glu Ser Lys Phe Tyr Lys Met Met Gln Gly Gly Val Gly
 50 55 60

Ile Pro Ser Ile Lys Trp Cys Gly Ala Glu Gly Asp Tyr Asn Val Met
 65 70 75 80

Val Met Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys
 85 90 95

Ser Arg Lys Phe Ser Leu Lys Thr Val Leu Leu Leu Ala Asp Gln Met
100 105 110

Ile Ser Arg Ile Glu Tyr Ile His Ser Lys Asn Phe Ile His Arg Asp
115 120 125

Val Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Lys Lys Gly Asn Leu
130 135 140

Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Ala Arg
145 150 155 160

Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
165 170 175

Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
180 185 190

Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met Tyr Phe Asn Leu
195 200 205

Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Ala Thr Lys Arg Gln Lys
210 215 220

Tyr Glu Arg Ile Ser Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu
225 230 235 240

Cys Lys Gly Tyr Pro Ser Glu Phe Ser Thr Tyr Leu Asn Phe Cys Arg
245 250 255

Ser Leu Arg Phe Asp Asp Lys Pro Asp Tyr Ser Tyr Leu Arg Gln Leu
260 265 270

Phe Arg Asn Leu Phe His Arg Gln Gly Phe Ser Tyr Asp Tyr Val Phe
275 280 285

Asp Trp Asn Met Leu Lys Phe Gly Ala Ala Arg Asn Pro Glu Asp Val
290 295 300

Asp Arg Glu Arg Arg Glu His Glu Arg Glu Glu Arg Met Gly Gln Leu
305 310 315 320

Arg Gly Ser Ala Thr Arg Ala Leu Pro Pro Gly Pro Pro Thr Gly Ala
 325 330 335

Thr Ala Asn Arg Leu Arg Ser Ala Ala Glu Pro Val Ala Ser Thr Pro
 340 345 350

Ala Ser Arg Ile Gln Pro Ala Gly Asn Thr Ser Pro Arg Ala Ile Ser
 355 360 365

Arg Val Asp Arg Glu Arg Lys Val Ser Met Arg Leu His Arg Gly Ala
 370 375 380

Pro Ala Asn Val Ser Ser Ser Asp Leu Thr Gly Arg Gln Glu Val Ser
 385 390 395 400

Arg Ile Pro Ala Ser Gln Thr Ser Val Pro Phe Asp His Leu Gly Lys
 405 410 415

<210> 11
 <211> 1559
 <212> DNA
 <213> Homo sapiens

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cggcggctc cgcaatccct cggcatccg cccggcggg ccgcggccgc ccgcggcagc	240
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acgtgtgggg aacaagtacc gcctgggacg gaagatcggg agcgggtcct tcggagatat	360
ctacctgggt gccaacatca cctctggta ggaagtgcgc atcaagctgg agtgtgtgaa	420
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ggggatcccg tccatcaagt ggtgcggagc tgagggcgac tacaacgtga tggtcatgga	540
gctgctgggg cctagcctcg aggacctgtt caacttctgt tcccgcaaat tcagcctcaa	600
gacggtgctg ctcttggccg accagatgtat cagccgcattc gaggatatcc actccaagaa	660
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<210> 12
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<400> 12

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Ser Gly Ser Phe Gly Asp Ile Tyr Leu Gly Ala Asn Ile Thr Ser Gly
 20 25 30

Glu Glu Val Ala Ile Lys Leu Glu Cys Val Lys Thr Lys His Pro Gln
 35 40 45

Leu His Ile Glu Ser Lys Phe Tyr Lys Met Met Gln Gly Gly Val Gly
 50 55 60

Ile Pro Ser Ile Lys Trp Cys Gly Ala Glu Gly Asp Tyr Asn Val Met
 65 70 75 80

Val Met Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys
 85 90 95

Ser Arg Lys Phe Ser Leu Lys Thr Val Leu Leu Leu Ala Asp Gln Met
100 105 110

Ile Ser Arg Ile Glu Tyr Ile His Ser Lys Asn Phe Ile His Arg Asp
115 120 125

Val Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Lys Lys Gly Asn Leu
130 135 140

Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr Arg Asp Ala Arg
145 150 155 160

Thr His Gln His Ile Pro Tyr Arg Glu Asn Lys Asn Leu Thr Gly Thr
165 170 175

Ala Arg Tyr Ala Ser Ile Asn Thr His Leu Gly Ile Glu Gln Ser Arg
180 185 190

Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met Tyr Phe Asn Leu
195 200 205

Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Ala Thr Lys Arg Gln Lys
210 215 220

Tyr Glu Arg Ile Ser Glu Lys Lys Met Ser Thr Pro Ile Glu Val Leu
225 230 235 240

Cys Lys Gly Tyr Pro Ser Glu Phe Ser Thr Tyr Leu Asn Phe Cys Arg
245 250 255

Ser Leu Arg Phe Asp Asp Lys Pro Asp Tyr Ser Tyr Leu Arg Gln Leu
260 265 270

Phe Arg Asn Leu Phe His Arg Gln Gly Phe Ser Tyr Asp Tyr Val Phe
275 280 285

Asp Trp Asn Met Leu Lys Phe Gly Ala Ala Arg Asn Pro Glu Asp Val
290 295 300

Asp Arg Glu Arg Arg Glu His Glu Arg Glu Glu Arg Met Gly Gln Leu
305 310 315 320

Arg Gly Ser Ala Thr Arg Ala Leu Pro Pro Gly Pro Pro Thr Gly Ala
325 330 335

Thr Ala Asn Arg Leu Arg Ser Ala Ala Glu Pro Val Ala Ser Thr Pro
340 345 350

Ala Ser Arg Ile Gln Pro Ala Gly Asn Thr Ser Pro Arg Ala Ile Ser
355 360 365

Arg Val Asp Arg Glu Arg Lys Val Ser Met Arg Leu His Arg Gly Ala
370 375 380

Pro Ala Asn Val Ser Ser Ser Asp Leu Thr Gly Arg Gln Glu Val Ser
385 390 395 400

Arg Ile Pro Ala Ser Gln Thr Ser Val Pro Phe Asp His Leu Gly Lys
405 410 415